

SEQUENCE LISTING

<110> Alexandra Charlesworth
 Falvia Spirito
 Guerrino Meneguzzi
 John Baird
 Keith Linder

<120> ISOLATION OF THE LAMININ Y2 GENE IN
 HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS
 BULLOSA

<130> p84us4

<160> 32

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3989

<212> DNA

<213> equine

<220>

<221> CDS

<222> (198)...(3767)

<223>

<400> 1

```

cggtcctcc ttattcacag gtgagtcaca ccctgaaaca caggctctct tcctgtcagg      60
actgagtcag gtagaagagt cgataaaacc acctgatcaa ggaaaaggaa ggcacagcgg      120
agcgagaggt gagaactccc agcggcgagg cgccgggcag cgaccctgc agcggcggac      180
cgcgcgccgg cctggcc atg cct gcg ctc tgg ctg agc tgc tac ctc tgc      230
                Met Pro Ala Leu Trp Leu Ser Cys Tyr Leu Cys
                  1                5                10

ctc tgc ctc ctc ctg ccc gca gcc cgg gcc acc tcc ggg agg gaa gtc      278
Phe Ser Leu Leu Leu Pro Ala Ala Arg Ala Thr Ser Gly Arg Glu Val
                15                20                25

tgt gat tgc aac ggg aag tcc agg caa tgc atc ttt gac cag gaa ctt      326
Cys Asp Cys Asn Gly Lys Ser Arg Gln Cys Ile Phe Asp Gln Glu Leu
                30                35                40

cac aaa cag aca gga aat gga ttc cgc tgc ctc aac tgc aat gac aac      374
His Lys Gln Thr Gly Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn
                45                50                55

act gat ggc atc cac tgc gag agg tgc aag gca gga ttt tac cga cag      422
Thr Asp Gly Ile His Cys Glu Arg Cys Lys Ala Gly Phe Tyr Arg Gln
        60                65                70                75

aga gaa agg gac cgc tgt tta ccc tgc aat tgt aac tct aaa ggt tct      470
Arg Glu Arg Asp Arg Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser
                80                85                90
  
```

ctt agc gct cga tgt gac aac tct gga cgg tgc agc tgt aag cca ggt	518
Leu Ser Ala Arg Cys Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly	
95 100 105	
gtg aca gga gac agg tgt gac cga tgt ctg ccc ggc ttc cac aca ctc	566
Val Thr Gly Asp Arg Cys Asp Arg Cys Leu Pro Gly Phe His Thr Leu	
110 115 120	
act gat gct ggg tgc gcc caa gac caa agg ctg cta gac tcc aag tgt	614
Thr Asp Ala Gly Cys Ala Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys	
125 130 135	
gac tgt gac cca gct ggc atc tca ggg ccc tgt gac tca ggc cgc tgt	662
Asp Cys Asp Pro Ala Gly Ile Ser Gly Pro Cys Asp Ser Gly Arg Cys	
140 145 150 155	
gtc tgc aag ccg gct gtc act gga gag cgc tgt gat agg tgt cga cca	710
Val Cys Lys Pro Ala Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Pro	
160 165 170	
ggg tac tat cac ctg gat ggg gga aac cct cag ggc tgt acc cag tgt	758
Gly Tyr Tyr His Leu Asp Gly Gly Asn Pro Gln Gly Cys Thr Gln Cys	
175 180 185	
ttt tgc tat ggg cat tcc gcc agc tgc cac agc tct ggg gac tac agt	806
Phe Cys Tyr Gly His Ser Ala Ser Cys His Ser Ser Gly Asp Tyr Ser	
190 195 200	
gtc cat aaa atc atc tct gcc ttc cat caa gat gtt gat ggc tgg aag	854
Val His Lys Ile Ile Ser Ala Phe His Gln Asp Val Asp Gly Trp Lys	
205 210 215	
gct gtc caa aga aac ggg tct cct gca aag ctc cag tgg tca cag cgc	902
Ala Val Gln Arg Asn Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg	
220 225 230 235	
cat cgg gat ata ttt agc tca gca cga cga tca gac cct gtc tat ttt	950
His Arg Asp Ile Phe Ser Ser Ala Arg Arg Ser Asp Pro Val Tyr Phe	
240 245 250	
gta gct cct gcc aaa ttt ctt ggg aat caa cag gtg agc tac ggg caa	998
Val Ala Pro Ala Lys Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln	
255 260 265	
agc cta tct ttt gac tac cgt gtg gat agg gga ggc aga cac cca tct	1046
Ser Leu Ser Phe Asp Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser	
270 275 280	
gcc cat gac gtg atc ctg gaa ggt gct ggt cta cgg atc aca gct ccc	1094
Ala His Asp Val Ile Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro	
285 290 295	
ttg atg cca ctt agc aag aca ctg cct tgt ggg atc acc aag act tac	1142
Leu Met Pro Leu Ser Lys Thr Leu Pro Cys Gly Ile Thr Lys Thr Tyr	
300 305 310 315	

aca ttc aga tta aat gaa cat cca agc agt aat tgg agc ccc cag cta	1190
Thr Phe Arg Leu Asn Glu His Pro Ser Ser Asn Trp Ser Pro Gln Leu	
320 325 330	
agt tac ttt gag tat cgg agg tta ctg cgg aac ctc aca gcc ctg cgg	1238
Ser Tyr Phe Glu Tyr Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg	
335 340 345	
atc cga gct acc tac gga gaa tac agt act ggg tac att gac aac gtg	1286
Ile Arg Ala Thr Tyr Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val	
350 355 360	
acc ttg att tca gcc cgc ccc gtt tct gga gcc cca gcg ccc tgg gtt	1334
Thr Leu Ile Ser Ala Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val	
365 370 375	
gaa caa tgt gta tgc cct gtt ggc tac aag ggg cag ttc tgc cag gat	1382
Glu Gln Cys Val Cys Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp	
380 385 390 395	
tgt gct tcc ggc tac aaa aga gat tca gcc aga ctg gga cct ttt ggc	1430
Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly	
400 405 410	
cc tgt att cca tgt aac tgc caa ggg gga ggg gcc tgc gat cca gac	1478
Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp	
415 420 425	
aca gga gac tgt tac tca ggg gat gag aac cct gac atc cct gag tgt	1526
Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn Pro Asp Ile Pro Glu Cys	
430 435 440	
act gac tgc ccc att ggt ttc tac aac gat cca caa gac ccc cgc agc	1574
Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro Gln Asp Pro Arg Ser	
445 450 455	
ggc aag ccg tgc ccc tgt cgc aat ggg ttc agc tgc tcc gtg atg cct	1622
Cys Lys Pro Cys Pro Cys Arg Asn Gly Phe Ser Cys Ser Val Met Pro	
460 465 470 475	
gag aca gag gag gtg gtg tgc aat aac tgc ccc cag ggt gtc act ggt	1670
Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro Gln Gly Val Thr Gly	
480 485 490	
gcc cgc tgt gag ctc tgt gct gat ggc tat ttt ggg gac ccc ttc ggg	1718
Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly	
495 500 505	
gaa cgt ggc cca gtg agg cct tgt cag ccc tgt cag tgc aac aac aac	1766
Glu Arg Gly Pro Val Arg Pro Cys Gln Pro Cys Gln Cys Asn Asn Asn	
510 515 520	
gtg gac cct agt gcc tcc ggg aac tgt gac cgc ctg aca ggc agg tgt	1814
Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys	
525 530 535	
ctg aag tgc atc cac aac aca gct ggg gtc cac tgt gac cag tgc aaa	1862

Leu	Lys	Cys	Ile	His	Asn	Thr	Ala	Gly	Val	His	Cys	Asp	Gln	Cys	Lys	
540					545					550					555	
gca	ggc	tac	tat	ggg	gac	ccg	ttg	gct	ccc	aat	cca	gca	gac	aag	tgt	1910
Ala	Gly	Tyr	Tyr	Gly	Asp	Pro	Leu	Ala	Pro	Asn	Pro	Ala	Asp	Lys	Cys	
				560					565					570		
cga	gct	tgc	aac	tgc	aac	cca	gtg	ggc	tcg	gag	cct	gtg	gag	tgt	cga	1958
Arg	Ala	Cys	Asn	Cys	Asn	Pro	Val	Gly	Ser	Glu	Pro	Val	Glu	Cys	Arg	
			575					580					585			
agt	gat	ggc	agc	tgt	gtt	tgc	aag	cca	ggc	ttt	ggg	ggc	ctc	agc	tgt	2006
Ser	Asp	Gly	Ser	Cys	Val	Cys	Lys	Pro	Gly	Phe	Gly	Gly	Leu	Ser	Cys	
		590					595					600				
gag	cat	gcg	gca	ctg	acc	agc	tgt	cca	gct	tgc	tat	aat	caa	gtg	aag	2054
Glu	His	Ala	Ala	Leu	Thr	Ser	Cys	Pro	Ala	Cys	Tyr	Asn	Gln	Val	Lys	
	605					610					615					
gtt	cag	atg	gat	cag	ttt	atg	cag	cag	ctc	cag	atc	ctg	gag	gcc	ctg	2102
Val	Gln	Met	Asp	Gln	Phe	Met	Gln	Gln	Leu	Gln	Ile	Leu	Glu	Ala	Leu	
620					625				630						635	
ttt	tcg	aag	gct	cag	ggg	gga	gca	gta	ccc	aac	gca	gag	ctg	gaa	ggc	2150
Ile	Ser	Lys	Ala	Gln	Gly	Gly	Ala	Val	Pro	Asn	Ala	Glu	Leu	Glu	Gly	
				640					645					650		
agg	atg	cag	cag	gct	gag	cag	gcc	ctt	cgg	gac	att	ctg	aga	gaa	gcc	2198
Arg	Met	Gln	Gln	Ala	Glu	Gln	Ala	Leu	Arg	Asp	Ile	Leu	Arg	Glu	Ala	
			655					660					665			
cag	att	tca	caa	gat	gct	gtt	aga	tcc	ttc	aat	ctc	cgg	gtg	gcc	aag	2246
Gln	Ile	Ser	Gln	Asp	Ala	Val	Arg	Ser	Phe	Asn	Leu	Arg	Val	Ala	Lys	
		670					675					680				
gca	agg	act	caa	gag	aat	agc	tac	cgg	gac	cgc	ctg	gat	gac	ctc	aag	2294
Ala	Arg	Thr	Gln	Glu	Asn	Ser	Tyr	Arg	Asp	Arg	Leu	Asp	Asp	Leu	Lys	
	685					690					695					
atg	act	gtg	gaa	aga	gtt	cgg	gcc	ctg	ggc	agt	cag	tat	cag	aac	caa	2342
Met	Thr	Val	Glu	Arg	Val	Arg	Ala	Leu	Gly	Ser	Gln	Tyr	Gln	Asn	Gln	
700					705					710					715	
gtt	cag	gat	act	cgc	agg	ctc	atc	act	cag	atg	cgc	ctg	agc	ctg	gag	2390
Val	Gln	Asp	Thr	Arg	Arg	Leu	Ile	Thr	Gln	Met	Arg	Leu	Ser	Leu	Glu	
				720					725					730		
gaa	agt	gag	gct	tcc	ctg	caa	aac	acc	aac	att	cct	cct	tca	gag	cac	2438
Glu	Ser	Glu	Ala	Ser	Leu	Gln	Asn	Thr	Asn	Ile	Pro	Pro	Ser	Glu	His	
			735					740					745			
tac	gtg	ggg	cca	aat	ggc	ttt	aaa	agt	ctg	gct	cag	gag	gcc	acg	aga	2486
Tyr	Val	Gly	Pro	Asn	Gly	Phe	Lys	Ser	Leu	Ala	Gln	Glu	Ala	Thr	Arg	
		750					755					760				
ttg	gca	gac	agc	cat	gtt	cag	tca	gcc	agt	aac	atg	gag	caa	ctg	gca	2534
Leu	Ala	Asp	Ser	His	Val	Gln	Ser	Ala	Ser	Asn	Met	Glu	Gln	Leu	Ala	

765	770	775	
aag gaa acc cag gag tat tcc aaa gag ctg atg tca ctg gtg cgc gag Lys Glu Thr Gln Glu Tyr Ser Lys Glu Leu Met Ser Leu Val Arg Glu 780 785 790 795			2582
gct ctg cag gaa gga ggc gga agc ggc agc ctg gac gga gcc gtg gtg Ala Leu Gln Glu Gly Gly Gly Ser Gly Ser Leu Asp Gly Ala Val Val 800 805 810			2630
caa agg ctt gtg gga aaa ttg cag aaa act aaa tct ctg gcc cag gag Gln Arg Leu Val Gly Lys Leu Gln Lys Thr Lys Ser Leu Ala Gln Glu 815 820 825			2678
ttg tcg agg gag gcc acg caa acc gac atg gaa gca gat agg tct tat Leu Ser Arg Glu Ala Thr Gln Thr Asp Met Glu Ala Asp Arg Ser Tyr 830 835 840			2726
cag cat agt ctc cac ctt ctc aat tcc gtg tct cag att cag gga gtc Gln His Ser Leu His Leu Leu Asn Ser Val Ser Gln Ile Gln Gly Val 845 850 855			2774
aat gat cag tcc ttg cag gta gaa gcg aag agg ctc aga caa aaa gct Asn Asp Gln Ser Leu Gln Val Glu Ala Lys Arg Leu Arg Gln Lys Ala 860 865 870 875			2822
aat tct ctc tca aac cgt gtg act aag cat atg gat gag ttc aag cac asp Ser Leu Ser Asn Arg Val Thr Lys His Met Asp Glu Phe Lys His 880 885 890			2870
gtg caa agc aat ctg gga aac tgg gaa gaa gaa acc cgg cag ctc tta Val Gln Ser Asn Leu Gly Asn Trp Glu Glu Glu Thr Arg Gln Leu Leu 895 900 905			2918
cag aat gga aag aat ggg aga cag aca tca gat cag ctg ctt tcc cgt Gln Asn Gly Lys Asn Gly Arg Gln Thr Ser Asp Gln Leu Leu Ser Arg 910 915 920			2966
gcc aac ctt gct aaa agc aga gcc caa gaa gca cta agt atg ggc aat Ala Asn Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn 925 930 935			3014
gcc act ttt tat gaa gtt gag aac atc tta aag aat ctc aga gag ttt Ala Thr Phe Tyr Glu Val Glu Asn Ile Leu Lys Asn Leu Arg Glu Phe 940 945 950 955			3062
gac ctg cag gtt gga gat aaa aga gca gaa gct gaa gag gcc atg aag Asp Leu Gln Val Gly Asp Lys Arg Ala Glu Ala Glu Glu Ala Met Lys 960 965 970			3110
aga ctc tcc tac atc agc cag aag gtt gca ggt gcc agt gac aag acg Arg Leu Ser Tyr Ile Ser Gln Lys Val Ala Gly Ala Ser Asp Lys Thr 975 980 985			3158
aag caa gca gaa gca gcc ctg ggc agt gct gct gcc gac gcc cag agg Lys Gln Ala Glu Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg 990 995 1000			3206

gca aag aat gca gcc agg gag gcc ctg gag atc tct ggc aag ata gaa	3254
Ala Lys Asn Ala Ala Arg Glu Ala Leu Glu Ile Ser Gly Lys Ile Glu	
1005 1010 1015	
cag gag ata gga ggt ctg aac ttg gaa gcc aat gtg aca gca gat gga	3302
Gln Glu Ile Gly Gly Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly	
1020 1025 1030 1035	
gcc ttg gcc atg gag aag gga ctg gcc act ctg aaa agt gag atg aga	3350
Ala Leu Ala Met Glu Lys Gly Leu Ala Thr Leu Lys Ser Glu Met Arg	
1040 1045 1050	
gaa gtg gaa gga gag ctg tca agg aag gag cag gag ttt gac atg gat	3398
Glu Val Glu Gly Glu Leu Ser Arg Lys Glu Gln Glu Phe Asp Met Asp	
1055 1060 1065	
atg gac gca gtg cag atg gta att gca gag gcc caa aga gtt gaa aac	3446
Met Asp Ala Val Gln Met Val Ile Ala Glu Ala Gln Arg Val Glu Asn	
1070 1075 1080	
aga gcc aag aat gct gga gtt acg atc caa gac aca ctc aac aca ttg	3494
Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu	
1085 1090 1095	
gat ggc atc cta cac cta ata gac cag cct ggc agt gtg gat gaa gag	3542
Asp Gly Ile Leu His Leu Ile Asp Gln Pro Gly Ser Val Asp Glu Glu	
1100 1105 1110 1115	
agg ctg atc tta ctg gag cag aag ctt ttc cga gcc aag act cag atc	3590
Arg Leu Ile Leu Leu Glu Gln Lys Leu Phe Arg Ala Lys Thr Gln Ile	
1120 1125 1130	
aac agc cag cta cgg ccc ttg atg tca gag ctg gaa gag agg gca cat	3638
Asn Ser Gln Leu Arg Pro Leu Met Ser Glu Leu Glu Glu Arg Ala His	
1135 1140 1145	
egg cag aag ggc cac ctc cgt ttc ctg gag act agc ata gat ggg att	3686
Arg Gln Lys Gly His Leu Arg Phe Leu Glu Thr Ser Ile Asp Gly Ile	
1150 1155 1160	
ctg gct gat gtg aag aac ctg gag aac atc agg gac aac ctg ccc ccg	3734
Leu Ala Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro	
1165 1170 1175	
ggc tgc tac aat acc cag gct ctt gag caa cag tgaagctgcc ttagagattt	3787
Gly Cys Tyr Asn Thr Gln Ala Leu Glu Gln	
1180 1185 1190	
ctcaaccaag gttcttggga ttcagaccta gctgccttag agattttctca accaagggttc	3847
ttgggattca gacctcaggg ctcaggagcc cgcattgcggg tgggggtggga tgggaatatt	3907
tgaatatgtt gaatgcgtgt gctcaggccc cagtgaacct gatcccatcc ctgagacctc	3967
ggccagataa atgtctttat tg	3989
<210> 2	
<211> 1190	
<212> PRT	

<213> Equine

<220>

<223>

<400> 2

Met Pro Ala Leu Trp Leu Ser Cys Tyr Leu Cys Phe Ser Leu Leu Leu
1 5 10 15
Pro Ala Ala Arg Ala Thr Ser Gly Arg Glu Val Cys Asp Cys Asn Gly
20 25 30
Lys Ser Arg Gln Cys Ile Phe Asp Gln Glu Leu His Lys Gln Thr Gly
35 40 45
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
50 55 60
Cys Glu Arg Cys Lys Ala Gly Phe Tyr Arg Gln Arg Glu Arg Asp Arg
65 70 75 80
Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
85 90 95
Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Asp Arg
100 105 110
Cys Asp Arg Cys Leu Pro Gly Phe His Thr Leu Thr Asp Ala Gly Cys
115 120 125
Ala Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
130 135 140
Gly Ile Ser Gly Pro Cys Asp Ser Gly Arg Cys Val Cys Lys Pro Ala
145 150 155 160
Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Pro Gly Tyr Tyr His Leu
165 170 175
Asp Gly Gly Asn Pro Gln Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
180 185 190
Ser Ala Ser Cys His Ser Ser Gly Asp Tyr Ser Val His Lys Ile Ile
195 200 205
Ser Ala Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
210 215 220
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Arg Asp Ile Phe
225 230 235 240
Ser Ser Ala Arg Arg Ser Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
245 250 255
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
260 265 270
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
275 280 285
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Ser
290 295 300
Lys Thr Leu Pro Cys Gly Ile Thr Lys Thr Tyr Thr Phe Arg Leu Asn
305 310 315 320
Glu His Pro Ser Ser Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
325 330 335
Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
340 345 350
Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
355 360 365
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Val Cys
370 375 380
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385 390 395 400
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys

405 410 415
 Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
 420 425 430
 Ser Gly Asp Glu Asn Pro Asp Ile Pro Glu Cys Ala Asp Cys Pro Ile
 435 440 445
 Gly Phe Tyr Asn Asp Pro Gln Asp Pro Arg Ser Cys Lys Pro Cys Pro
 450 455 460
 Cys Arg Asn Gly Phe Ser Cys Ser Val Met Pro Glu Thr Glu Glu Val
 465 470 475 480
 Val Cys Asn Asn Cys Pro Gln Gly Val Thr Gly Ala Arg Cys Glu Leu
 485 490 495
 Cys Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu Arg Gly Pro Val
 500 505 510
 Arg Pro Cys Gln Pro Cys Gln Cys Asn Asn Asn Val Asp Pro Ser Ala
 515 520 525
 Ser Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His
 530 535 540
 Asn Thr Ala Gly Val His Cys Asp Gln Cys Lys Ala Gly Tyr Tyr Gly
 545 550 555 560
 Asp Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys
 565 570 575
 Asn Pro Val Gly Ser Glu Pro Val Glu Cys Arg Ser Asp Gly Ser Cys
 580 585 590
 Val Cys Lys Pro Gly Phe Gly Gly Leu Ser Cys Glu His Ala Ala Leu
 595 600 605
 Thr Ser Cys Pro Ala Cys Tyr Asn Gln Val Lys Val Gln Met Asp Gln
 610 615 620
 Phe Met Gln Gln Leu Gln Ile Leu Glu Ala Leu Ile Ser Lys Ala Gln
 625 630 635 640
 Gly Gly Ala Val Pro Asn Ala Glu Leu Glu Gly Arg Met Gln Gln Ala
 645 650 655
 Glu Gln Ala Leu Arg Asp Ile Leu Arg Glu Ala Gln Ile Ser Gln Asp
 660 665 670
 Ala Val Arg Ser Phe Asn Leu Arg Val Ala Lys Ala Arg Thr Gln Glu
 675 680 685
 Asn Ser Tyr Arg Asp Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
 690 695 700
 Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Gln Val Gln Asp Thr Arg
 705 710 715 720
 Arg Leu Ile Thr Gln Met Arg Leu Ser Leu Glu Glu Ser Glu Ala Ser
 725 730 735
 Leu Gln Asn Thr Asn Ile Pro Pro Ser Glu His Tyr Val Gly Pro Asn
 740 745 750
 Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Asp Ser His
 755 760 765
 Val Gln Ser Ala Ser Asn Met Glu Gln Leu Ala Lys Glu Thr Gln Glu
 770 775 780
 Tyr Ser Lys Glu Leu Met Ser Leu Val Arg Glu Ala Leu Gln Glu Gly
 785 790 795 800
 Gly Gly Ser Gly Ser Leu Asp Gly Ala Val Val Gln Arg Leu Val Gly
 805 810 815
 Lys Leu Gln Lys Thr Lys Ser Leu Ala Gln Glu Leu Ser Arg Glu Ala
 820 825 830
 Thr Gln Thr Asp Met Glu Ala Asp Arg Ser Tyr Gln His Ser Leu His
 835 840 845
 Leu Leu Asn Ser Val Ser Gln Ile Gln Gly Val Asn Asp Gln Ser Leu
 850 855 860

Gln Val Glu Ala Lys Arg Leu Arg Gln Lys Ala Asp Ser Leu Ser Asn
 865 870 875 880
 Arg Val Thr Lys His Met Asp Glu Phe Lys His Val Gln Ser Asn Leu
 885 890 895
 Gly Asn Trp Glu Glu Glu Thr Arg Gln Leu Leu Gln Asn Gly Lys Asn
 900 905 910
 Gly Arg Gln Thr Ser Asp Gln Leu Leu Ser Arg Ala Asn Leu Ala Lys
 915 920 925
 Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr Phe Tyr Glu
 930 935 940
 Val Glu Asn Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu Gln Val Gly
 945 950 955 960
 Asp Lys Arg Ala Glu Ala Glu Glu Ala Met Lys Arg Leu Ser Tyr Ile
 965 970 975
 Ser Gln Lys Val Ala Gly Ala Ser Asp Lys Thr Lys Gln Ala Glu Ala
 980 985 990
 Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys Asn Ala Ala
 995 1000 1005
 Arg Glu Ala Leu Glu Ile Ser Gly Lys Ile Glu Gln Glu Ile Gly Gly
 1010 1015 1020
 Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly Ala Leu Ala Met Glu
 1025 1030 1035 1040
 Lys Gly Leu Ala Thr Leu Lys Ser Glu Met Arg Glu Val Glu Gly Glu
 1045 1050 1055
 Leu Ser Arg Lys Glu Gln Glu Phe Asp Met Asp Met Asp Ala Val Gln
 1060 1065 1070
 Met Val Ile Ala Glu Ala Gln Arg Val Glu Asn Arg Ala Lys Asn Ala
 1075 1080 1085
 Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly Ile Leu His
 1090 1095 1100
 Leu Ile Asp Gln Pro Gly Ser Val Asp Glu Glu Arg Leu Ile Leu Leu
 1105 1110 1115 1120
 Glu Gln Lys Leu Phe Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg
 1125 1130 1135
 Pro Leu Met Ser Glu Leu Glu Glu Arg Ala His Arg Gln Lys Gly His
 1140 1145 1150
 Leu Arg Phe Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys
 1155 1160 1165
 Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr
 1170 1175 1180
 Gln Ala Leu Glu Gln Gln
 1185 1190

<210> 3
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 3
 atgcctgcgc tctggctcag

20

<210> 4
 <211> 20
 <212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 4

tgtggcagct ggcggaatgc

20

<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 5

gactccaagt gtgactgtga

20

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 6

gagctcacct gttgattccc

20

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 7

cctgtctatt ttgtagctcc

20

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 8

cagctgaacc cattgcgaca

20

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>	
<223> primer	
<400> 9	
gagtatcgga gggtactgcg	20
<210> 10	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 10	
gacactccac aggctccgag	20
<210> 11	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 11	
ggctgtgagc tctgtgctga	20
<210> 12	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 12	
ctccaggatc tggagctgct	20
<210> 13	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 13	
gacaagtgtc gagcttgcaa	20
<210> 14	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	

<400> 14	
tcatcatgag gtcatccagg	20
<210> 15	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 15	
gagagaagcc cagatttcac	20
<210> 16	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 16	
gcttccatgt cggtttgcgt	20
<210> 17	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 17	
cagccagtaa catggagcaa	20
<210> 18	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 18	
gtctgtctcc cattctttcc	20
<210> 19	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 19	

ggatgagttc aagcacgtgc	20
<210> 20	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 20	
acagctctcc ttccacttct	20
<210> 21	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 21	
caagacgaag caagcagaag	20
<210> 22	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 22	
ggctgttgat ctgagtcttg	20
<210> 23	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 23	
gtgagtcaca ccctgaaaca	20
<210> 24	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 24	
gagttacaat tgcagggtac ac	22

<210> 25
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 25
 ggccatgcgt agactcttaa tttttttttt tttttt 36

 <210> 26
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 26
 gcagaggccc aaagagttg 19

 <210> 27
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 27
 ggccatgcgt agactcttaa 20

 <210> 28
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 28
 cctggcagtg tggatgaaga 20

 <210> 29
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 29
 tggtactcag gggatgagaa 20

 <210> 30
 <211> 19

<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 30
ctgggggcag ttattgcac

19

<210> 31
<211> 1193
<212> PRT
<213> human

<220>
<223>

<400> 31

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
1 5 10 15
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
20 25 30
Cys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
35 40 45
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
50 55 60
Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
65 70 75 80
Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
85 90 95
Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
100 105 110
Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
115 120 125
Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
130 135 140
Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145 150 155 160
Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
165 170 175
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
180 185 190
Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
195 200 205
Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
210 215 220
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225 230 235 240
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
245 250 255
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
260 265 270
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
275 280 285
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
290 295 300
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn

305					310					315				320
Glu	His	Pro	Ser	Asn	Asn	Trp	Ser	Pro	Gln	Leu	Ser	Tyr	Phe	Glu
				325					330					335
Arg	Arg	Leu	Leu	Arg	Asn	Leu	Thr	Ala	Leu	Arg	Ile	Arg	Ala	Thr
				340					345					350
Gly	Glu	Tyr	Ser	Thr	Gly	Tyr	Ile	Asp	Asn	Val	Thr	Leu	Ile	Ser
				355				360						365
Arg	Pro	Val	Ser	Gly	Ala	Pro	Ala	Pro	Trp	Val	Glu	Gln	Cys	Ile
				370				375						380
Pro	Val	Gly	Tyr	Lys	Gly	Gln	Phe	Cys	Gln	Asp	Cys	Ala	Ser	Gly
					390					395				400
Lys	Arg	Asp	Ser	Ala	Arg	Leu	Gly	Pro	Phe	Gly	Thr	Cys	Ile	Pro
				405					410					415
Asn	Cys	Gln	Gly	Gly	Gly	Ala	Cys	Asp	Pro	Asp	Thr	Gly	Asp	Cys
				420				425						430
Ser	Gly	Asp	Glu	Asn	Pro	Asp	Ile	Glu	Cys	Ala	Asp	Cys	Pro	Ile
				435				440						445
Phe	Tyr	Asn	Asp	Pro	His	Asp	Pro	Arg	Ser	Cys	Lys	Pro	Cys	Pro
						455						460		Cys
His	Asn	Gly	Phe	Ser	Cys	Ser	Val	Met	Pro	Glu	Thr	Glu	Glu	Val
						470				475				480
Cys	Asn	Asn	Cys	Pro	Pro	Gly	Val	Thr	Gly	Ala	Arg	Cys	Glu	Leu
				485					490					495
Ala	Asp	Gly	Tyr	Phe	Gly	Asp	Pro	Phe	Gly	Glu	His	Gly	Pro	Val
				500				505					510	Arg
Pro	Cys	Gln	Pro	Cys	Gln	Cys	Asn	Asn	Asn	Val	Asp	Pro	Ser	Ala
				515				520						525
Gly	Asn	Cys	Asp	Arg	Leu	Thr	Gly	Arg	Cys	Leu	Lys	Cys	Ile	His
						535								540
Thr	Ala	Gly	Ile	Tyr	Cys	Asp	Gln	Cys	Lys	Ala	Gly	Tyr	Phe	Gly
						550				555				560
Pro	Leu	Ala	Pro	Asn	Pro	Ala	Asp	Lys	Cys	Arg	Ala	Cys	Asn	Cys
				565					570					575
Pro	Met	Gly	Ser	Glu	Pro	Val	Gly	Cys	Arg	Ser	Asp	Gly	Thr	Cys
				580					585					590
Cys	Lys	Pro	Gly	Phe	Gly	Gly	Pro	Asn	Cys	Glu	His	Gly	Ala	Phe
				595				600						605
Cys	Pro	Ala	Cys	Tyr	Asn	Gln	Val	Lys	Ile	Gln	Met	Asp	Gln	Phe
						615								620
Gln	Gln	Leu	Gln	Arg	Met	Glu	Ala	Leu	Ile	Ser	Lys	Ala	Gln	Gly
					630					635				640
Asp	Gly	Val	Val	Pro	Asp	Thr	Glu	Leu	Glu	Gly	Arg	Met	Gln	Gln
				645					650					655
Glu	Gln	Ala	Leu	Gln	Asp	Ile	Leu	Arg	Asp	Ala	Gln	Ile	Ser	Glu
				660					665					670
Ala	Ser	Arg	Ser	Leu	Gly	Leu	Gln	Leu	Ala	Lys	Val	Arg	Ser	Gln
				675				680						685
Asn	Ser	Tyr	Gln	Ser	Arg	Leu	Asp	Asp	Leu	Lys	Met	Thr	Val	Glu
						695								700
Val	Arg	Ala	Leu	Gly	Ser	Gln	Tyr	Gln	Asn	Arg	Val	Arg	Asp	Thr
					710					715				720
Arg	Leu	Ile	Thr	Gln	Met	Gln	Leu	Ser	Leu	Ala	Glu	Ser	Glu	Ala
				725						730				735
Leu	Gly	Asn	Thr	Asn	Ile	Pro	Ala	Ser	Asp	His	Tyr	Val	Gly	Pro
				740				745						750
Gly	Phe	Lys	Ser	Leu	Ala	Gln	Glu	Ala	Thr	Arg	Leu	Ala	Glu	Ser
				755				760						765

Val	Glu	Ser	Ala	Ser	Asn	Met	Glu	Gln	Leu	Thr	Arg	Glu	Thr	Glu	Asp
770						775					780				
Tyr	Ser	Lys	Gln	Ala	Leu	Ser	Leu	Val	Arg	Lys	Ala	Leu	His	Glu	Gly
785					790					795					800
Val	Gly	Ser	Gly	Ser	Gly	Ser	Pro	Asp	Gly	Ala	Val	Val	Gln	Gly	Leu
				805					810					815	
Val	Glu	Lys	Leu	Glu	Lys	Thr	Lys	Ser	Leu	Ala	Gln	Gln	Leu	Thr	Arg
			820					825					830		
Glu	Ala	Thr	Gln	Ala	Glu	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser
		835					840					845			
Leu	Arg	Leu	Leu	Asp	Ser	Val	Ser	Arg	Leu	Gln	Gly	Val	Ser	Asp	Gln
	850					855					860				
Ser	Phe	Gln	Val	Glu	Glu	Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser
865					870					875					880
Leu	Ser	Thr	Leu	Val	Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln
				885					890					895	
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn
			900					905					910		
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn
		915					920						925		
Leu	Ala	Lys	Ser	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr
	930					935					940				
Phe	Tyr	Glu	Val	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu
945					950					955					960
Gln	Val	Asp	Asn	Arg	Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu
				965					970					975	
Ser	Tyr	Ile	Ser	Gln	Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln
			980					985					990		
Ala	Glu	Arg	Ala	Leu	Gly	Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys
		995					1000					1005			
Asn	Gly	Ala	Gly	Glu	Ala	Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu
	1010					1015					1020				
Ile	Gly	Ser	Leu	Asn	Leu	Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu
	1025				1030					1035					1040
Ala	Met	Glu	Lys	Gly	Leu	Ala	Ser	Leu	Lys	Ser	Glu	Met	Arg	Glu	Val
				1045					1050					1055	
Glu	Gly	Glu	Leu	Glu	Arg	Lys	Glu	Leu	Glu	Phe	Asp	Thr	Asn	Met	Asp
		1060					1065					1070			
Ala	Val	Gln	Met	Val	Ile	Thr	Glu	Ala	Gln	Lys	Val	Asp	Thr	Arg	Ala
		1075					1080					1085			
Lys	Asn	Ala	Gly	Val	Thr	Ile	Gln	Asp	Thr	Leu	Asn	Thr	Leu	Asp	Gly
	1090					1095					1100				
Leu	Leu	His	Leu	Met	Asp	Gln	Pro	Leu	Ser	Val	Asp	Glu	Glu	Gly	Leu
1105					1110					1115					1120
Val	Leu	Leu	Glu	Gln	Lys	Leu	Ser	Arg	Ala	Lys	Thr	Gln	Ile	Asn	Ser
				1125					1130					1135	
Gln	Leu	Arg	Pro	Met	Met	Ser	Glu	Leu	Glu	Glu	Arg	Ala	Arg	Gln	Gln
			1140					1145				1150			
Arg	Gly	His	Leu	His	Leu	Leu	Glu	Thr	Ser	Ile	Asp	Gly	Ile	Leu	Ala
		1155					1160				1165				
Asp	Val	Lys	Asn	Leu	Glu	Asn	Ile	Arg	Asp	Asn	Leu	Pro	Pro	Gly	Cys
	1170					1175					1180				
Tyr	Asn	Thr	Gln	Ala	Leu	Glu	Gln	Gln							
1185					1190										

<210> 32

<211> 1192

<212> PRT
<213> murine

<220>
<223>

<400> 32

Met	Pro	Ala	Leu	Trp	Leu	Ser	Cys	Cys	Leu	Gly	Val	Ala	Leu	Leu	Leu
1			5						10					15	
Pro	Ala	Ser	Gln	Ala	Thr	Ser	Arg	Arg	Glu	Val	Cys	Asp	Cys	Asn	Gly
			20					25					30		
Lys	Ser	Arg	Gln	Cys	Val	Phe	Asp	Gln	Glu	Leu	His	Arg	Gln	Ala	Gly
		35					40					45			
Ser	Gly	Phe	Arg	Cys	Leu	Asn	Cys	Asn	Asp	Asn	Thr	Ala	Gly	Val	His
	50					55					60				
Cys	Glu	Arg	Ser	Arg	Glu	Gly	Phe	Tyr	Gln	His	Gln	Ser	Lys	Ser	Arg
65					70				75						80
Cys	Leu	Pro	Cys	Asn	Cys	His	Ser	Lys	Gly	Ser	Leu	Ser	Ala	Gly	Cys
				85					90					95	
Asp	Asn	Ser	Gly	Gln	Cys	Arg	Cys	Lys	Pro	Gly	Val	Thr	Gly	Gln	Arg
			100					105					110		
Cys	Asp	Gln	Cys	Gln	Pro	Gly	Phe	His	Met	Leu	Thr	Asp	Ala	Gly	Cys
			115				120					125			
Thr	Arg	Asp	Gln	Gly	Gln	Leu	Asp	Ser	Lys	Cys	Asp	Cys	Asp	Pro	Ala
	130					135					140				
Gly	Ile	Ser	Gly	Pro	Cys	Asp	Ser	Gly	Arg	Cys	Val	Cys	Lys	Pro	Ala
145					150					155					160
Val	Thr	Gly	Glu	Arg	Cys	Asp	Arg	Cys	Arg	Pro	Arg	Asp	Tyr	His	Leu
				165					170					175	
Asp	Arg	Ala	Asn	Pro	Glu	Gly	Cys	Thr	Gln	Cys	Phe	Cys	Tyr	Gly	His
			180					185					190		
Ser	Ala	Ser	Cys	His	Ala	Ser	Ala	Asp	Phe	Ser	Val	His	Lys	Ile	Thr
		195					200					205			
Ser	Thr	Phe	Ser	Gln	Asp	Val	Asp	Gly	Trp	Lys	Ala	Val	Gln	Arg	Asn
	210				215						220				
Gly	Ala	Pro	Ala	Lys	Leu	His	Trp	Ser	Gln	Arg	His	Arg	Asp	Val	Phe
225					230					235					240
Ser	Ser	Ala	Arg	Arg	Ser	Asp	Pro	Val	Tyr	Phe	Val	Ala	Pro	Ala	Lys
				245					250					255	
Phe	Leu	Gly	Asn	Gln	Gln	Val	Ser	Tyr	Gly	Gln	Ser	Leu	Ser	Phe	Asp
			260					265					270		
Tyr	Arg	Val	Asp	Arg	Gly	Gly	Arg	Gln	Pro	Ser	Ala	Tyr	Asp	Val	Ile
		275					280					285			
Leu	Glu	Gly	Ala	Gly	Leu	Gln	Ile	Arg	Ala	Pro	Leu	Met	Ala	Pro	Gly
	290					295					300				
Lys	Thr	Leu	Pro	Cys	Gly	Ile	Thr	Lys	Thr	Tyr	Thr	Phe	Arg	Leu	Asn
305					310					315					320
Glu	His	Pro	Ser	Ser	His	Trp	Ser	Pro	Gln	Leu	Ser	Tyr	Phe	Glu	Tyr
				325					330					335	
Arg	Arg	Leu	Leu	Arg	Asn	Leu	Thr	Ala	Leu	Leu	Met	Ile	Arg	Ala	Thr
			340					345					350		
Tyr	Gly	Glu	Tyr	Ser	Thr	Gly	Tyr	Ile	Asp	Asn	Val	Thr	Leu	Val	Ser
		355				360						365			
Ala	Arg	Pro	Val	Leu	Gly	Ala	Pro	Ala	Pro	Trp	Val	Glu	Arg	Cys	Val
	370					375					380				
Cys	Leu	Leu	Gly	Tyr	Lys	Gly	Gln	Phe	Cys	Gln	Glu	Cys	Ala	Ser	Gly
385					390					395					400

Tyr Lys Arg Asp Ser Ala Arg Leu Gly Ala Phe Gly Ala Cys Val Pro
 405 410 415
 Cys Asn Cys Gln Gly Glu Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys
 420 425 430
 Tyr Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile
 435 440 445
 Gly Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro
 450 455 460
 Cys His Asn Gly Phe Ser Cys Ser Val Met Pro Glu Thr Glu Glu Val
 465 470 475 480
 Val Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu
 485 490 495
 Cys Ala Asp Gly Phe Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val
 500 505 510
 Arg Pro Cys Gln Arg Cys Gln Cys Asn Asn Asn Val Asp Pro Asn Ala
 515 520 525
 Ser Gly Asn Cys Asp Gln Leu Thr Gly Arg Cys Leu Lys Cys Ile Tyr
 530 535 540
 Asn Thr Ala Gly Val Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly
 545 550 555 560
 Asp Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys
 565 570 575
 Ser Pro Met Gly Ala Glu Pro Gly Glu Cys Arg Gly Asp Gly Ser Cys
 580 585 590
 Val Cys Lys Pro Gly Phe Gly Ala Phe Asn Cys Asp His Ala Ala Leu
 595 600 605
 Thr Ser Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln
 610 615 620
 Phe Thr Gln Gln Leu Gln Ser Leu Glu Ala Leu Val Ser Lys Ala Gln
 625 630 635 640
 Gly Gly Gly Gly Gly Gly Thr Val Pro Val Gln Leu Glu Gly Arg Ile
 645 650 655
 Glu Gln Ala Glu Gln Ala Leu Gln Asp Ile Leu Gly Glu Ala Gln Ile
 660 665 670
 Ser Glu Gly Ala Met Arg Ala Val Ala Val Arg Leu Ala Lys Ala Arg
 675 680 685
 Ser Gln Glu Asn Asp Tyr Lys Thr Arg Leu Asp Asp Leu Lys Met Thr
 690 695 700
 Ala Glu Arg Ile Arg Ala Leu Gly Ser Gln His Gln Asn Arg Val Gln
 705 710 715 720
 Asp Thr Ser Arg Leu Ile Ser Gln Met Arg Leu Ser Leu Ala Gly Ser
 725 730 735
 Glu Ala Leu Leu Glu Asn Thr Asn Ile His Ser Ser Glu His Tyr Val
 740 745 750
 Gly Pro Asn Asp Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Lys Ala
 755 760 765
 Asp Ser His Ala Glu Ser Ala Asn Ala Met Lys Gln Leu Ala Arg Glu
 770 775 780
 Thr Glu Asp Tyr Ser Lys Gln Ala Leu Ser Leu Ala Arg Lys Leu Leu
 785 790 795 800
 Ser Gly Gly Gly Gly Ser Gly Ser Trp Asp Ser Ser Val Val Gln Gly
 805 810 815
 Leu Met Gly Lys Leu Glu Lys Thr Lys Ser Leu Ser Gln Gln Leu Ser
 820 825 830
 Leu Glu Gly Thr Gln Ala Asp Ile Glu Ala Asp Arg Ser Tyr Gln His
 835 840 845
 Ser Leu Arg Leu Leu Asp Ser Ala Ser Gln Leu Gln Gly Val Ser Asp

850	855	860
Leu Ser Phe Gln Val	Glu Ala Lys Arg Ile	Arg Gln Lys Ala Asp Ser
865	870	875
Leu Ser Asn Leu Val	Thr Arg Gln Thr Asp	Ala Phe Thr Arg Val Arg
	885	890
Asn Asn Leu Gly Asn Trp	Glu Lys Glu Thr Arg	Gln Leu Leu Gln Thr
	900	905
Gly Lys Asp Arg Arg	Gln Thr Ser Asp	Gln Leu Leu Ser Arg Ala Asn
	915	920
Leu Ala Lys Asn Arg	Ala Gln Glu Ala Leu Ser	Met Gly Asn Ala Thr
	930	935
Phe Tyr Glu Val Glu	Asn Ile Leu Lys Asn	Leu Arg Glu Phe Asp Leu
	945	950
Gln Val Glu Asp Arg	Lys Ala Glu Ala Glu	Glu Ala Met Lys Arg Leu
	965	970
Ser Ser Ile Ser Gln	Lys Val Ala Asp	Ala Ser Asp Lys Thr Gln Gln
	980	985
Ala Glu Thr Ala Leu	Gly Ser Ala Thr Ala	Asp Thr Gln Arg Ala Lys
	995	1000
Asn Ala Ala Arg Glu	Ala Leu Glu Ile Ser	Ser Glu Ile Glu Leu Glu
	1010	1015
Ile Gly Ser Leu Asn	Leu Glu Ala Asn Val	Thr Ala Asp Gly Ala Leu
	1025	1030
Ala Met Glu Lys Gly	Thr Ala Thr Leu Lys	Ser Glu Met Arg Glu Met
	1045	1050
Ile Glu Leu Ala Arg	Lys Glu Leu Glu Phe	Asp Thr Asp Lys Asp Thr
	1060	1065
Val Gln Leu Val Ile	Thr Glu Ala Gln Gln	Ala Asp Ala Arg Ala Thr
	1075	1080
Ser Ala Gly Val Thr	Ile Gln Asp Thr Leu	Asn Thr Leu Asp Gly Ile
	1090	1095
Leu His Leu Ile Asp	Gln Pro Gly Ser Val	Asp Glu Glu Gly Met Met
	1105	1110
Leu Leu Glu Gln Gly	Leu Phe Gln Ala Lys	Thr Gln Ile Asn Ser Arg
	1125	1130
Leu Arg Pro Leu Met	Ser Asp Leu Glu Arg	Val Arg Arg Gln Arg
	1140	1145
Asn His Leu His Leu	Glu Thr Ser Ile Asp	Gly Ile Leu Ala Asp
	1155	1160
Val Lys Asn Leu Glu	Asn Ile Arg Asp	Asn Leu Pro Pro Gly Cys Tyr
	1170	1175
Asn Thr Gln Ala Leu	Glu Gln Gln	
	1185	1190